AMENDMENT TO THE CLAIMS

1-40. (Canceled)

41. (Currently Amended) The method of ~~claim 38~~ claim 54 wherein the reporter system comprises a reporter gene which is operably linked to a sequence of nucleotides that provides a binding site for p53 or for a protein that associates with, or is a substrate for, p53.

42. (Previously Presented) The method of claim 41 wherein the reporter gene is operably linked to a p21 or Bax promoter.

43. (Previously Presented) The method of claim 41 wherein the protein product of the reporter gene includes a secretion signal peptide.

44. (Previously Presented) The method of claim 41 wherein the protein product of the reporter gene includes a transmembrane domain.

45. (Previously Presented) The method of claim 41 wherein the host cells have been transfected with the reporter gene.

46-47. (Canceled)

48. (Currently Amended) The method of ~~claim 38~~ claim 54, wherein the library is introduced into the host cells in the form of nucleic acid constructs which encode the peptide library.

49. (Currently Amended) The method of ~~claim 38~~ claim 54, wherein each peptide encoded by the library of nucleic acid constructs ~~member of the peptide library~~ has the sequence M-G/M/V-(X)n, wherein n is an integer from 3 to 6, M is methionine, G is glycine, V is valine and each X, which may be the same or different, is any genetically coded amino acid.

50. (Currently Amended) The method of ~~claim 38~~ claim 54, wherein the library of nucleic acid constructs ~~peptide library has~~ encodes for at least 500 different ~~members~~ peptides.

51. (Currently Amended) The method of ~~claim 38~~ claim 54 wherein the host cells are eukaryotic cells.

52-53. (Withdrawn)

54. (Currently Amended) A method of identifying a peptide of 2 to 8 amino acids in length having the ability to restore ~~or modify~~ the wild type the function of p53 in an intra-cellular environment comprising:

(a) introducing a library comprising nucleic acid constructs encoding peptides of 2 to 8 amino acids in length into host cells having a reporter system that allows for the identification of those cells in which the wild type function of p53 has been restored ~~or modified~~;

(b) identifying a cell in which the wild type function of p53 has been restored ~~or modified~~; and

(c) identifying the peptide in the cell of step (b).

55. (Currently Amended) A method of identifying a peptide of 2 to 8 amino acids in length having the ability to restore ~~or modify~~ the wild type function of p53 in an intra-cellular environment comprising:

(a) introducing a library comprising peptides of 2 to 8 amino acids in length into host cells having a reporter system that allows for the identification of those cells in which the function of p53 has been restored ~~or modified~~;

(b) identifying a cell in which the function of p53 has been restored ~~or modified~~;

and

(c) identifying the peptide in the cell of step (b).

56. (New) The method of claim 55 wherein the reporter system comprises a reporter gene which is operably linked to a sequence of nucleotides that provides a binding site for p53 or for a protein that associates with, or is a substrate for, p53.

57. (New) The method of claim 56 wherein the reporter gene is operably linked to a p21 or Bax promoter.

58. (New) The method of claim 56 wherein the protein product of the reporter gene includes a secretion signal peptide.

59. (New) The method of claim 56 wherein the protein product of the reporter gene includes a transmembrane domain.

60. (New) The method of claim 56 wherein the host cells have been transfected with the reporter gene.

61. (New) The method of claim 55, wherein each member of the peptide library has the sequence M-G/M/V-(X)n, wherein n is an integer from 3 to 6, M is methionine, G is glycine, V is valine and each X, which may be the same or different, is any genetically coded amino acid.

62. (New) The method of claim 55, wherein the peptide library has at least 500 different members.

63. (New) The method of claim 55 wherein the host cells are eukaryotic cells.